

SEQUENCE LISTING

<110> Boehringer Ingelheim Pharma KG

<120> Method for identifying compounds which positively influence inflammatory conditions

<130> 1/1177

<140>

<141>

<150> US 60/257,854

<151> 2000-12-22

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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<210> 2

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 2

gtcgtcaaga tgctaccgtt cagga 25

<210> 3

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 3

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ccagaaattt ctctctccatc tgattttgag cacaccatcc atgttggtt tgatactggt 180
actggagaat tcaactggcat gccagaacag tgggtctgat tactacagac ctccaatc 240
accaaactag agcaaaagaa gaatcctcag gctgtgctgg atgtcctaaa gttcctacag 300
tccaacacag tgaagcagaa atatctgagc ttactcctc ctgagaaaaa tggctttcct 360
tctggaacac cagcactgaa tgccaaggga acagaagcac ccgcagtagt gacagaggag 420

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gatgggtgctg ccaagtcttt agacaaacag aaaaagaaga ctaagatgac agatgaagag 600
attatgggaga aattaagaac tatcgtgagc ataggtgacc ctaagaaaaa atatacaaga 660
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agttacctgg taggagatga attgtttgtg gtcattggaat acctgtctgg gaggtcactc 900
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gacaatgtac ttttgggaat ggaaggatct gttaagctca ctgactttgg tttctgtgcc 1080
cagatcacc ctagcagag caaacgcagt accatggctg gaacgccata ctggatggca 1140
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agacaaccaa gagaaaattg caaaaagaca agtatgactt ttatatgaac ccottcttta 1680
gggtccagaa ggaattgtgg actgaatcac tagccttagg tctttcagca aacagcctat 1740
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<210> 4
 <211> 524
 <212> PRT
 <213> Homo sapiens

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 Ala Asn His Ser Leu Lys Pro Leu Pro Ser Val Pro Glu Glu Lys Lys
 35 40 45
 Pro Arg His Lys Ile Ile Ser Ile Phe Ser Gly Thr Glu Lys Gly Ser
 50 55 60
 Lys Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Pro Pro Ser Asp Phe
 65 70 75 80
 Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe Thr
 85 90 95
 Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile Thr
 100 105 110
 Lys Leu Glu Gln Lys Lys Asn Pro Gln Ala Val Leu Asp Val Leu Lys
 115 120 125
 Phe Tyr Asp Ser Asn Thr Val Lys Gln Lys Tyr Leu Ser Phe Thr Pro

130		135		140
Pro Glu Lys Asp Gly Leu	Pro Ser Gly Thr	Pro Ala Leu Asn Ala Lys		
145	150	155	160	
Gly Thr Glu Ala Pro Ala Val Val Thr	Glu Glu Glu Asp Asp Asp Glu			
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Glu Thr Ala Pro Pro Val Ile Ala Pro Arg Pro Asp His Thr Lys Ser				
	180	185	190	
Ile Tyr Thr Arg Ser Val Ile Asp Pro Val Pro Ala Pro Val Gly Asp				
	195	200	205	
Ser His Val Asp Gly Ala Ala Lys Ser Leu Asp Lys Gln Lys Lys Lys				
	210	215	220	
Pro Lys Met Thr Asp Glu Glu Ile Met Glu Lys Leu Arg Thr Ile Val				
225	230	235	240	
Ser Ile Gly Asp Pro Lys Lys Lys Tyr Thr Arg Tyr Glu Lys Ile Gly				
	245	250	255	
Gln Gly Ala Ser Gly Thr Val Phe Thr Ala Thr Asp Val Ala Leu Gly				
	260	265	270	
Gln Glu Val Ala Ile Lys Gln Ile Asn Leu Gln Lys Gln Pro Lys Lys				
	275	280	285	
Glu Leu Ile Ile Asn Glu Ile Leu Val Met Lys Glu Leu Lys Asn Pro				
	290	295	300	
Asn Ile Val Asn Phe Leu Asp Ser Tyr Leu Val Gly Asp Glu Leu Phe				
	305	310	315	320
Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu Thr Asp Val Val Thr				
	325	330	335	
Glu Thr Cys Met Asp Glu Ala Gln Ile Ala Ala Val Cys Arg Glu Cys				
	340	345	350	
Leu Gln Ala Leu Glu Phe Leu His Ala Asn Gln Val Ile His Arg Asp				
	355	360	365	
Ile Lys Ser Asp Asn Val Leu Leu Gly Met Glu Gly Ser Val Lys Leu				
	370	375	380	
Thr Asp Phe Gly Phe Cys Ala Gln Ile Thr Pro Glu Gln Ser Lys Arg				
	385	390	395	400
Ser Thr Met Val Gly Thr Pro Tyr Trp Met Ala Pro Glu Val Val Thr				
	405	410	415	
Arg Lys Ala Tyr Gly Pro Lys Val Asp Ile Trp Ser Leu Gly Ile Met				
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 8

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29

<210> 9

<211> 3255

<212> DNA

<213> Homo sapiens

<400> 9

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gatacaatgg	tgacgcagaa	attggatgat	atcaaggatc	gaattaagag	agaaataaag	180
aaagaactcg	aaatcaaaag	aggagctgaa	aatctgagga	aagtcacaa	agataaaaaa	240
agtttggctt	atgtagacaa	cattttgaaa	aaatcaaaat	aaaaattaga	agaactacat	300
cacaagctgc	aggaattaaa	tgacacatatt	gttgtatcag	atccagaaga	tattacagat	360
tgcccaagg	ctccagatgc	tccaaataat	gacctctgtt	gttctactag	caacaataga	420
ttgaaggcct	tacaaaaaca	attggatata	gaacttaaa	taaaacaagg	tgacagagat	480
atgatcacga	tgtattcaaa	tgatcttcca	aaggatcgga	aactccatgg	tacagctcag	540
caactgtctc	aggaacagca	gacaaaaata	gaagtcatgc	gaatgcagat	tcttcaggca	600
gtccagagata	atgaattggc	ttttgataat	gcaaaacctg	tgataagtc	tcttgaactt	660
cggttggaag	aattaaaggca	tcattttagg	atagagtttg	cagtagcaga	aggtgcaaa	720
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caagcaagat	ttaattgaatc	aagtcagaag	ttggaccttt	taaagtattc	attagagcaa	840
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<210> 10

<211> 984

<212> PRT

<213> Homo sapiens

<400> 10

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Met Ala Ser Asn Pro Glu Arg Gly Glu Ile Leu Leu Thr Glu Leu Gln
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             20             25             30

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Lys Leu Asp Phe Ser Asp Thr Met Val Gln Gln Lys Leu Asp Asp Ile
  35             40             45

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Lys Asp Arg Ile Lys Arg Glu Ile Arg Lys Glu Leu Lys Ile Lys Glu
  50             55             60

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Gly Ala Glu Asn Leu Arg Lys Val Thr Thr Asp Lys Lys Ser Leu Ala
  65             70             75             80

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Tyr Val Asp Asn Ile Leu Lys Lys Ser Asn Lys Lys Leu Glu Glu Leu
  85             90             95

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His His Lys Leu Gln Glu Leu Asn Ala His Ile Val Val Ser Asp Pro
 100             105             110

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Glu Asp Ile Thr Asp Cys Pro Arg Thr Pro Asp Thr Pro Asn Asn Asp
 115             120             125

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Pro Arg Cys Ser Thr Ser Asn Asn Arg Leu Lys Ala Leu Gln Lys Gln
 130             135             140

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Leu Asp Ile Glu Leu Lys Val Lys Gln Gly Ala Glu Asn Met Ile Gln
 145             150             155             160

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Met Tyr Ser Asn Gly Ser Ser Lys Asp Arg Lys Leu His Gly Thr Ala
 165             170             175

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Gln Gln Leu Leu Gln Asp Ser Lys Thr Lys Ile Glu Val Ile Arg Met
 180             185             190

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Lys	Leu	Leu	Gly	Ser	Gly	Lys	Val	Thr	Asp	Arg	Lys	Ala	Leu	Ser	Glu		
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Ala	Gln	Ala	Arg	Phe	Asn	Glu	Ser	Ser	Gln	Lys	Leu	Asp	Leu	Leu	Lys		
		260						265					270				
Tyr	Ser	Leu	Glu	Gln	Arg	Leu	Asn	Glu	Val	Pro	Lys	Asn	His	Pro	Lys		
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Ser	Arg	Ile	Ile	Ile	Glu	Glu	Leu	Ser	Leu	Val	Ala	Ala	Ser	Pro	Thr		
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305					310					315					320		
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Ser	Val	Ala	Leu	Pro	Gly	Trp	Ser	Pro	Ser	Glu	Thr	Arg	Ser	Ser	Phe		
	355						360					365					
Met	Ser	Arg	Thr	Ser	Lys	Ser	Lys	Ser	Gly	Ser	Ser	Arg	Asn	Leu	Leu		
	370					375						380					
Lys	Thr	Asp	Asp	Leu	Ser	Asn	Asp	Val	Cys	Ala	Val	Leu	Lys	Leu	Asp		
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			405						410					415			
Trp	Asp	Gln	Lys	Phe	Thr	Leu	Glu	Leu	Asp	Arg	Ser	Arg	Glu	Leu	Glu		
		420						425					430				
Ile	Ser	Val	Tyr	Trp	Arg	Asp	Trp	Arg	Ser	Leu	Cys	Ala	Val	Lys	Phe		
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Tyr	Leu	Glu	Pro	Gln	Gly	Thr	Leu	Phe	Ala	Glu	Val	Thr	Phe	Phe	Asn		
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Pro	Val	Ile	Glu	Arg	Arg	Pro	Lys	Leu	Gln	Arg	Gln	Lys	Lys	Ile	Phe		
			485					490						495			

Ser	Lys	Gln	Gln	Gly	Lys	Thr	Phe	Leu	Arg	Ala	Pro	Gln	Met	Asn	Ile	
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Asn	Ile	Ala	Thr	Trp	Gly	Arg	Leu	Val	Arg	Arg	Ala	Ile	Pro	Thr	Val	
	515						520					525				
Asn	His	Ser	Gly	Thr	Phe	Ser	Pro	Gln	Ala	Pro	Val	Pro	Thr	Thr	Val	
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Pro	Val	Val	Asp	Val	Arg	Ile	Pro	Gln	Leu	Ala	Pro	Pro	Ala	Ser	Asp	
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Ser	Thr	Val	Thr	Lys	Leu	Asp	Phe	Asp	Leu	Glu	Pro	Glu	Pro	Pro	Pro	
			565						570				575			
Ala	Pro	Pro	Arg	Ala	Ser	Ser	Leu	Gly	Glu	Ile	Asp	Glu	Ser	Ser	Glu	
			580					585					590			
Leu	Arg	Val	Leu	Asp	Ile	Pro	Gly	Gln	Asp	Ser	Glu	Thr	Val	Phe	Asp	
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Ile	Gln	Asn	Asp	Arg	Asn	Ser	Ile	Leu	Pro	Lys	Ser	Gln	Ser	Glu	Tyr	
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Lys	Pro	Asp	Thr	Pro	Gln	Ser	Gly	Leu	Glu	Tyr	Ser	Gly	Ile	Gln	Glu	
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Phe	Arg	Cys	Cys	Ala	Val	Leu	Gly	Arg	Gly	His	Phe	Gly	Lys	Val	Leu	
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Leu	Ala	Glu	Tyr	Lys	Asn	Thr	Asn	Glu	Met	Phe	Ala	Ile	Lys	Ala	Leu	
	675						680					685				
Lys	Lys	Gly	Asp	Ile	Val	Ala	Arg	Asp	Glu	Val	Asp	Ser	Leu	Met	Cys	
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Glu	Lys	Arg	Ile	Phe	Glu	Thr	Val	Asn	Ser	Val	Arg	His	Pro	Phe	Leu	
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Val	Asn	Leu	Phe	Ala	Cys	Phe	Gln	Thr	Lys	Glu	His	Val	Cys	Phe	Val	
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Met	Glu	Tyr	Ala	Ala	Gly	Gly	Asp	Leu	Met	Met	His	Ile	His	Thr	Asp	
		740					745						750			
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	755						760					765				
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 Phe Cys Gly Thr Pro Glu Phe Leu Ala Pro Glu Val Leu Thr Glu Thr
 820 825 830
 Ser Tyr Thr Arg Ala Val Asp Trp Trp Gly Leu Gly Val Leu Ile Tyr
 835 840 845
 Glu Met Leu Val Gly Glu Ser Pro Phe Pro Gly Asp Asp Glu Glu Glu
 850 855 860
 Val Phe Asp Ser Ile Val Asn Asp Glu Val Arg Tyr Pro Arg Phe Leu
 865 870 875 880
 Ser Thr Glu Ala Ile Ser Ile Met Arg Arg Leu Leu Arg Arg Asn Pro
 885 890 895
 Glu Arg Arg Leu Gly Ala Ser Glu Lys Asp Ala Glu Asp Val Lys Lys
 900 905 910
 His Pro Phe Phe Arg Leu Ile Asp Trp Ser Ala Leu Met Asp Lys Lys
 915 920 925
 Val Lys Pro Pro Phe Ile Pro Thr Ile Arg Gly Arg Glu Asp Val Ser
 930 935 940
 Asn Phe Asp Asp Glu Phe Thr Ser Glu Ala Pro Ile Leu Thr Pro Pro
 945 950 955 960
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 965 970 975
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<210> 11

<211> 839

<212> DNA

<213> Homo sapiens

<400> 11

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<210> 12
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 <212> PRT
 <213> Homo sapiens

<400> 12

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Gly Phe Ser Val Ser His Thr Thr Arg Asn Pro Arg Pro Gly Glu Glu
 35 40 45

Asn Gly Lys Asp Tyr Tyr Phe Val Thr Arg Glu Val Met Gln Arg Asp
 50 55 60

Ile Ala Ala Gly Asp Phe Ile Glu His Ala Glu Phe Ser Gly Asn Leu
 65 70 75 80

Tyr Gly Thr Ser Lys Val Ala Val Gln Ala Val Gln Ala Met Asn Arg
 85 90 95

Ile Cys Val Leu Asp Val Asp Leu Gln Gly Val Arg Asn Ile Lys Ala
 100 105 110

Thr Asp Leu Arg Pro Ile Tyr Ile Ser Val Gln Pro Pro Ser Leu His
 115 120 125

Val Leu Glu Gln Arg Leu Arg Gln Arg Asn Thr Glu Thr Glu Glu Ser
 130 135 140

Leu Val Lys Arg Leu Ala Ala Ala Gln Ala Asp Met Glu Ser Ser Lys
 145 150 155 160

Glu Pro Gly Leu Phe Asp Val Val Ile Ile Asn Asp Ser Leu Asp Gln
 165 170 175

Ala Tyr Ala Glu Leu Lys Glu Ala Leu Ser Glu Glu Ile Lys Lys Ala
 180 185 190

Gln Arg Thr Gly Ala
 195

1

1